AMENDMENTS TO THE CLAIMS

1-13.   (cancelled)

14.   (currently amended) A method of designing a polyketide synthase (PKS) gene capable of producing a desired polyketide, which method comprises:

(a)   ~~defining a string of alphanumeric symbols representing the structure of said polyketide,~~

(b)   ~~comparing said string to a database of strings of alphanumeric symbols representing polyketides producible by PKS genes,~~

(c)   ~~identifying common elements in said string representing the structure of said desired polyketide with elements in said strings in said database, and~~

(d)   ~~generating and storing or displaying one or more new strings from elements identified in step (c) that have an exact match with said string representing the structure of said desired polyketide, wherein said new string defines a PKS gene capable of producing said desired polyketide~~

(a)   defining the structure of the desired polyketide by a first string of alphanumeric symbols, wherein each symbol in the first string represents a monomer unit of the polyketide,

(b)   comparing the first string to a second string from a database,

wherein the database comprises at least one second string of alphanumeric symbols representing a know polyketide, and wherein each symbol in the second string represents a monomer unit of the known polyketide and also represents a module of the polyketide synthase responsible for introducing the monomer unit into the known polyketide,

(c)   identifying a common symbol or continuous sequence of symbols in said first and second strings,

(d)   optionally repeating steps (b) and (c),

(e)   generating an alignment, wherein the alignment consists of a combination of common symbols identified from the database such that the sequence of symbols in the alignment

matches the first string, and wherein the alignment represents the structure of a new PKS gene capable of producing the desired polyketide, and

  (f) storing or displaying the alignment.

15. (currently amended) The method of claim 14, wherein ~~all possible PKS genes capable of producing the desired polyketide from said database are~~ more than one alignment is generated and displayed.

16. (currently amended) The method of claim [[14]] 15, wherein ~~said new strings generated in step (d)~~ the alignments that are generated are rated ~~and displayed~~ in an order based on one or more parameters.

17. (currently amended) The method of claim 16, wherein ~~said~~ the parameters are selected from the group consisting of a number of non-native module interfaces and a number of non-native protein interfaces.

18. (currently amended) A computer-readable medium embodying a set of program instructions configured to enable a computing device to perform method steps for designing a PKS gene capable of producing a desired polyketide, the method steps comprising:

  (a) ~~receiving a string of alphanumeric symbols representing the structure of said polyketide,~~

  (b) ~~comparing said string to a database of strings of alphanumeric symbols representing polyketides producible by PKS genes,~~

  (c) ~~identifying common elements in said string representing the structure of said desired polyketide with elements in said strings in said database, and~~

  (d) ~~generating and storing or displaying one or more new strings from elements identified in step (c) that have an exact match with said string representing the structure of said desired polyketide, wherein said new string defines a PKS gene capable of producing said desired polyketide~~

(a)   receiving a first string of alphanumeric symbols representing the structure of the desired polyketide, wherein each symbol in the first string represents a monomer unit of the desired polyketide,

(b)   comparing the first string to a second string from a database,

wherein the database comprises at least one second string of alphanumeric symbols representing a known polyketide, and wherein each symbol in the second string represents a monomer unit of the known polyketide and also represents a module of the polyketide synthase responsible for introducing the monomer unit into the known polyketide,

(c)   identifying a common symbol or continuous sequence of symbols in said first and second strings,

(d)   optionally repeating steps (b) and (c),

(e)   generating an alignment, wherein the alignment consists of a combination of common symbols identified from the database such that the sequence of symbols in the alignment matches the first string, and wherein the alignment represents the structure of a new PKS gene capable of producing the desired polyketide, and

(f)   storing or displaying the alignment.

19.   (currently amended) A computer-implemented method for designing a PKS gene capable of producing a desired polyketide comprising:

(a)   receiving a string of alphanumeric symbols representing the structure of said polyketide,

(b)   comparing said string to a database of strings of alphanumeric symbols representing polyketides producible by PKS genes,

(c)   identifying common elements in said string representing the structure of said desired polyketide with elements in said strings in said database, and

(d)   generating and storing or displaying one or more new strings from elements identified in step (c) that have an exact match with said string representing the structure of said desired polyketide, wherein said new string defines a PKS gene capable of producing said desired polyketide

sd-373816

(a)   receiving a first string of alphanumeric symbols representing the structure of the desired polyketide, wherein each symbol in the first string represents a monomer unit of the desired polyketide,

(b)   comparing the first string to a second string from a database,

wherein the database comprises at least one second string of alphanumeric symbols representing a known polyketide, and wherein each symbol in the second string represents a monomer unit of the known polyketide and also represents a module of the polyketide synthase responsible for introducing the monomer unit into the known polyketide,

(c)   identifying a common symbol or continuous sequence of symbols in said first and second strings,

(d)   optionally repeating steps (b) and (c),

(e)   generating an alignment, wherein the alignment consists of a combination of common symbols identified from the database such that the sequence of symbols in the alignment matches the first string, and wherein the alignment represents the structure of a new PKS gene capable of producing the desired polyketide, and

(f)   storing or displaying the alignment.

20.   (cancelled)

21.   (currently amended) The method of claim 14, wherein ~~all possible PKS genes capable of producing the desired polyketide from said database are~~ more than one alignment is generated and stored.

22.   (currently amended) The method of claim [[14]] 21, wherein ~~said new strings generated in step (d)~~ the alignments that are generated are rated ~~and stored~~ in an order based on one or more parameters.

23.   (new) The method of claim 22, wherein the parameters are selected from the group consisting of a number of non-native module interfaces and a number of non-native protein interfaces.

7

24.   (new) The alignment representing the structure of the new polyketides synthase (PKS) gene designed by the method of claim 14 or claim 19.